Amendments to the Specification

Please replace the paragraph beginning on page 17, line 3 with the following amended paragraph:

A method for depleting RNA species from nucleic acid samples is described. The method may be used, for example, for removing RNA species from cellular RNA samples such as blood. The blood sample may be isolated by any method. In some embodiments the methods are used for forensic analysis of blood. In particular the method may be used to remove globin mRNAs from samples derived from human blood. Applications include, for example, methods to increase the relative abundance of protein-encoding RNAs (mRNAs) by depleting the very abundant RNAs, such as ribosomal RNA, as disclosed in U.S. Patent No. 6,613,516 which is incorporated herein by reference in its entirety. General methods for depletion are also disclosed in U.S. Patent Nos. 6,040,138 and 6,391,592 which are both incorporated herein by reference in their entireties. For example, U.S. Patent No. 6,391,592 describes a method of blocking amplification of undesirable nucleic acids sequences during an amplification process by using blocking molecules to block synthesis of the complementary sequence. The blocking method may be used to block unwanted mRNA from being transcribed during in vitro reverse transcription of mRNA. The blocking molecule preferably hybridizes near the 3' end of the mRNA, preferably immediately upstream of the poly(A) tail of the unwanted mRNA. Blocking molecules may be, for example, peptide nucleic acids (PNAs), locked nucleic acids, RNA with a 3'-deoxyribonucleotide at the 3' end or DNA with a 2',3'-dideoxyribonucleotide at the 3' end.

Please replace the paragraph beginning on page 18, line 1 with the following amended paragraph:

In one embodiment a complementary single-stranded DNA "bait" molecule or "reduction oligo" is first hybridized to a region of a specific RNA that is complementary to the reduction oligo. In one embodiment the RNA component of the resulting RNA:DNA hybrid may then be hydrolyzed with an enzyme that is specific for RNA:DNA hybrids, for example, RNaseH. The DNA bait can be designed to hybridize to part or all of the RNA to be hydrolyzed. To sever the 3'-polyA tail from the rest of an mRNA, an oligonucleotide directed to a region upstream or 5' of the polyA tail may be used. In one embodiment the reduction oligo is hybridized to the region that is within ~~withing~~ 50, 100 or 200 bases of the 5' end of the poly(A) tail. Hybrids of greater length may be used to generate more extensive hydrolysis. Longer DNA bait could comprise, for example: multiple oligonucleotides hybridizing to different regions of the RNA to be hydrolyzed; single-stranded DNA made from phage carrying at least a portion of the sequence; denatured PCR product; denatured plasmid DNA containing at least a portion of the sequence; and complementary DNA made from the RNA molecules to be hydrolyzed using oligonucleotide primers and reverse transcriptase.